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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model		Run On:	December 1, 2002, 14:43:43 ; Search time 2658 Seconds (without alignments)	Score	Query Match	Length	DB ID	Description
Title:	US-09-680-959-125	Perfect score:	414	1 ctaaagtacagaacaaatggaccagg 414	1	384	92.8	Y15742 Mus musculus
Sequence:		Scoring table:	IDENTITY_NUC		2	384	92.8	BC030924 Mus musculus
		Gapop 10.0 , Gapext 1.0			3	384	92.8	AJ003407 Mus musculus
Se	ad:	2054640 seqs, 14551402878 residues	Total number of hits satisfying chosen parameters:	4109280	4	318.4	76.9	BC016655 Homo sapi
			Minimum DB seq length: 0		5	318.4	76.9	Y15722 Homo sapi
			Maximum DB seq length: 2000000000		6	318.4	76.9	Y12712 Homo sapi
			Post-processing: Minimum Match 0%		7	318.4	76.9	AF022728 Homo sapi
			Maximum Match 100%		8	318.4	76.9	Y15718 Homo sapi
			Listing first 45 summaries		9	316.8	76.5	AK094494 Homo sapi
Database :	GenBank:	1: gb_ba:*			10	202	48.8	AJ010206 Mus musculus
		2: gb_htg_*			11	189.4	45.7	LO6945 Torpedo californica
		3: gb_in:*			12	186.2	45.0	AF143542 Mus musculus
		4: gb_cm:*			13	186.2	45.0	X95227 M. musculus
		5: gb_ov:*			14	186.2	45.0	AF143544 Mus musculus
		6: gb_pat:*			15	186.2	45.0	X95226 M. musculus
		7: gb_ph:*			16	186.2	45.0	AF143543 Mus musculus
		8: gb_pl:*			17	183	44.2	AJ009668 Homo sapi
		9: gb_pr:*			18	183	44.2	U26742 Human dystrophin
		10: gb_ro:*			19	183	44.2	BC005300 Homo sapi
		11: gb_scs:*			20	183	44.2	U26744 Human dystrophin
		12: gb_sy:*			21	183	44.2	U46744 Human dystrophin
		13: gb_un:*			22	183	44.2	U46745 Human dystrophin
		14: gb_v1:*			23	183	44.2	AL833285 Homo sapi
		15: em_da:*			c	24	178	AC130150 Rattus norvegicus
		16: em_fun:*				25	157.2	AC130150 Rattus norvegicus
		17: em_num:*				26	150.8	AC010150 Homo sapi
		18: em_in:*				27	121.8	AF277387 Drosophila melanogaster
		19: em_mu:*				28	100.8	U279759 M. musculus
		20: em_om:*				29	99.8	U84531 Human dystrophin
		21: em_or:*				30	99.8	AC022601 Homo sapi
		22: em_ov:*				c	31	99.8
		23: em_pat:*				32	99.8	AC068506 Homo sapi
		24: em_pl:*				33	99.8	AP002411 Homo sapi
		25: em_ro:*				34	94.2	AC013832 Drosophila melanogaster
		26: em_scs:*				35	94.2	AC017911 Drosophila melanogaster
		27: em_sy:*				36	94.2	AC007476 Drosophila melanogaster
		28: em_un:*				37	94.2	AC007356 Drosophila melanogaster
		29: em_yi:*				38	88.6	AE003822 Drosophila melanogaster
		30: em_htg_hum:*				c	39	85.4
		31: em_htg_inv:*				40	72	MMU15742 mRNA for dystrobrevin B, partial.
		32: em_htg_other:*				41	60.2	AC010208 Mus musculus
		33: em_htg_mus:*				42	44.6	279790 M. musculus
		34: em_htg_pln:*				c	43	AC106483 Rattus norvegicus
		35: em_htg_rdn:*				44	10.6	AF098989 Caenorhabditis elegans
		36: em_htg_rnm:*				c	45	43.2
		37: em_sy:*				45	10.4	AF098989 Caenorhabditis elegans
		38: em_htg_yrt:*						AC006910 Caenorhabditis elegans
		39: em_htg_hum:*						
		40: em_htg_other:*						
		41: em_htg_other:*						

ALIGNMENTS

RESULT 1
MMU15742

LOCUS MMU15742 mRNA for dystrobrevin B, partial.

DEFINITION Mus musculus mRNA for dystrobrevin B.

ACCESSION Y15742

VERSION 1 GI:3127923

KEYWORDS

SOURCE Mus musculus

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2192)

AUTHORS Puca, A.A.

TITLE Direct Submission

JOURNAL Submitted (28-NOV-1997) A.A. Puca, T.I.G.E.M., Via Olgentina 58,

Pred. No. is the number of results predicted by chance to have a

RESULT	6	Qy	243	AATTTCATGGTCGCCCTTACGACACTGAGGCCAGGGCAGNTTGACCGTGTTCAGNT	302
LOCUS	HSDYSTRAO	2247 bp	trNA	Linear	PRI 29-MAY-1998
DEFINITION	Homo sapiens mRNA for brain dystrobrevin B.				
VERSION	Y12712				
KEYWORDS	GI:2765226				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. Pucca, A.A.				
AUTHORS	1 (bases 1 to 2247)				
TITLE	Direct Submission				
JOURNAL	Submitted (22-APR-1997) A.A. Pucca, Seconda Universita di Napoli, Istituto di Patologia Generale, Lorghetto S. Aniello a Caponapoli 2, Napoli 80138, Italy				
REF	INCEIORS	2 (bases 1 to 2247)			
FEATURES	Pucca, A.A., Nigro, V., Piluso, G., Belsito, A., Sampaolo, S., Quadrizi, N., Rossi, E., Di Iorio, G., Ballabio, A. and Franco, B.				
SOURCE	Identifies and characterizes a member of the dystrobrevin gene family and characterizes a novel member of the dystrobrevin gene family				
JOURNAL	FEBS Lett. 425 (1), 7-13 (1998)				
MEDLINE	98200066				
PUBMED	95409897				
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Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' - & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

Location/Qualifiers
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BASE COUNT
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Query Match
LocaL Similarity 76.5%; Score 316.8; DB 9; Length 2200;
bases 364; Conservative 0; Mismatches 46; Indels 2; Gaps 2;

QY 3 AACGTACAGAACAGCTTGCAGTTACCGATTGTCAGAACGGATGCAACCTCATCTTG 62
Db 225 AACTTACAGAACAGCTTGCAGTTACCGATTGTCAGAACGGATGCAACCTCATCTTG 283

QY 63 TTGATATCTGGATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 122

Db 284 TTGATATCTGGATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 402

QY 123 GCAAGGAGATAGGGCTGTCCGGCTTGAGAACGGCTCATCGTCATCATCGTCATCATCGT 182
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-QY 183 AACAAACGCCCTCCCTACTACCACTACAGATGTCAGCTGGAGCTGGAGTCAGCTCC 242

Db 403 AACAAACGCCCTCCCTACTACCACTACAGATGTCAGCTGGAGCTGGAGTCAGCTCC 462

QY 243 AATTTCATGGTCGCCCTACGACAGTCAGCTGGAGCTGGAGCTGGAGTCAGNT 302
Db 463 AACTTTATGATGGCTGAGCTGGAGCTGGAGCTGGAGCTGGAGCTGGATTTTCAGTT 522

QY 303 AAAGCTATGTTAGCAACCATGTTGGTGGAAAATGCTGGACAAATTGAGATACTATTTC 362
Db 523 AAAGCTATGTTAGCAACCATGTTGGTGGAAAATGCTGGACAAATTGAGATACTTTTC 582

QY 363 TCCCGATGTCAGATCCATGCTTAATGATGTTGAAAGCTGGAGCT 414
D' 583 TCCCGATGTCAGATCCATGCTTAATGATGTTGAAAGCTGGAGCT 634

RESULT 10
MM010206

LOCUS MM010206
DEFINITION Mus musculus beta-dystrobrevin gene, exon 3.
ACCESSION A010206
VERSION 1
KEYWORDS beta-dystrobrevin; dtn-b gene.
SOURCE Mus musculus.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Loh, N.Y. Direct Submission
Submitted (05-AUG-1998) Loh, N.Y., Genetics Unit, Department of Biochemistry, University of Oxford, South Parks Road, Oxford, OX1 3QU, UK

REFERENCE Loh, N.Y., Ambrose, H.J., Guay-Woodford, L.M., DasGupta, S., Nawrotzki, R.A., Blake, D.J. and Davies, K.E. Genomic organization and refined mapping of the mouse beta-dystrobrevin gene. Mamm. Genome 9 (11), 857-862 (1998)

FEATURES
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/organism="Mus musculus"
/db_xref="taxon:10090"
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/gene="dtn-b"
/number=3
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/usedin=A010202:dtn_mRNA_A
/usedin=A010203:dtn_mRNA_B
BASE COUNT
ORIGIN
84 a 109 c 70 g 117 t

Query Match
LocaL Similarity 48.4%; Score 202; DB 10; Length 380;
bases 213; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 54 TTCACTTGTGATATCTGGAAATATGATGCGAAAGCTTTCGGAGACATGGGCTTAACACGC 113
Db 84 TTCACTTGTGATATCTGGAAATATGATGCGAAAGCTTTCGGAGACATGGGCTTAACACGC 143
QY 114 TGGACCAACACAGAGATCAGGCTGTGTCAGCTGGAGACGGTCATCTGTCACTCTAC 173
Db 144 TGGACCAACACAGAGATCAGGCTGTGTCAGCTGGAGACGGTCATCTGTCACTCTAC 202
QY 174 TATCAGTTGACAAGGCTTCCCTCTACCTACCCAGATAGCTGGAGTCAGCTGGAG 233
Db 203 TATCAGTTGACAAGGCTTCCCTCTACCTACCCAGATAGCTGGAGTCAGCTGGAG 262
QY 234 CTCTCTACTCAATTTCATGGTCGCCCTAGACAG 268
Db 263 CTCTCTACTCAATTTCATGGTCGCCCTAGACAG 297

RESULT 11
FSCTRYDS
LOCUS FSCTRYDS
DEFINITION FSCTRYDS
ACCESSION L06945..1
VERSION GI:213244
KEYWORDS postsynaptic membrane protein.
SOURCE Torpedo californica (library: lambda gt11) adult electric organ cDNA
ORGANISM Torpedo californica
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Squalea; Hypnosqualea; Pristioraja; Batoidae; Torpediniformes; Torpedinidae; Torpedinidae; Torpedo.
REFERENCE 1 (bases 1 to 4615)
AUTHORS Wagner, K.R., Cohen, J.B. and Huganir, R.L.
TITLE The 87 k postsynaptic membrane protein from Torpedo is a protein-tyrosine kinase substrate homologous to dystrophin
JOURNAL Neuron 10 (3), 511-522 (1993)
MEDLINE 93213597
PUBMED 8461138
FEATURES Location/Qualifiers
source
/organism="Torpedo californica"
/db_xref="taxon:7787"
/tissue_type="electric organ"
/dev_stage="adult"
/tissue_lib="lambda gt11"
BASE COUNT 1507 a 836 c 893 g 1379 t
ORIGIN
Query Match
LocaL Similarity 45.7%; Score 189.4; DB 5;
Best Local Similarity 69.1%; Pred No. 1.8e-48;
Matches 284; Conservative 0; Mismatches 125; Indels 2; Gaps 2;

KEYWORDS 87 kDa protein; dystrobrevin.
 SOURCE Mus musculus.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 1 (bases 1 to 2607)
 REFERENCE Blak, D.J., Nawrotzki, R., Peters, M.F., Froehner, S.C. and
 Davies, K.E.
 AUTHORS Davies, K.E.
 TITLE Isoform diversity of dystrobrevin, the murine 87-kDa postsynaptic
 protein. J. Biol. Chem. 271 (13), 7802-7810 (1996)
 JOURNAL 86205975
 MEDLINE 861824
 PUBLMED 2 (bases 1 to 2607)
 AUTHORS Blak, D.J.
 TITLE Direct Submission
 JOURNAL Submitted (18-JAN-1996) D.J. Blak, Genetics Laboratory, Dep. of
 Biochemistry, Univ. of Oxford, South Park Road, Oxford, Oxfordshire
 OX1 3QU, UK
 FEATURES Location/Qualifiers
 source 1. 2607
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="24"
 /tissue="type: "brain"
 /dev_stage="adult"
 46. 2112
 /codon_start=1
 /product="dystrobrevin"
 /protein_id="CAA61518.1"
 /db_xref="GI:1246783"
 /db_xref="MGI:MGI:106039"
 /db_xref="SPREMBL:Q6198"
 /translation="MIEDSGKRGTAQMAERQLEAEMRAQDILRILSTYRACKLRFV
 QKICCNLHYDIVNTEALRNLNDNIELNARLPAVLSTIYOLNKRMPTTHQI
 HYVQSTISLLNEFLAEOFPEGHOKISVPAVKMNLATLGKKGMDKLYIESMISDSSG
 VWMYGRYDQFLREYLKLPIAVEBSPSFGTBEQARSCPSQKVTLNSFLDTLMSDPP
 POCUWLPPLHRLANVENPHYECSYCHSESNMGRYRCOOCHNYOLCQDCWWRGHA
 GGSHSNQHOMKETTSWSKSPAKLNLNLSKSLSCASSRPLHMPDQPEKPLNLAHTV
 PTOREVSMDTLESHSPVPSGSPPTIRSLRQELAELNKREELQEIQLRVEHQASQPPEKAQ
 NPTLAAEFLRILRQDKDELQORMSALESRELAYQLEGMLKKEEFLKQGPRASSPR
 SPSHTISRPIMPIRASACPTPHTQDLSLQVGGDQFAQFSSRNRLSLLVA
 ADSTNTNSSLVKEBLNSEVAYSEPTDSEPSRFQFEDIASPSPTSEAFQHRSRK
 GYTHGGAASTHGDMPDENGDPYQPEQNYENESVRQLENELQEEVKKQKQDEAV
 BASE COUNT 723 a 686 c 641 g 557 t
 ORIGIN
 very Match 45.0% Score 186.2; DB 10; Length 2607;
 ~ st Local Similarity 68.6%; Pred. No. 1.7e-47;
 ~ matches 282; Conservative 0; Mismatches 127; Indels 2; Gaps 2;
 QY 4 ACGTACAGAACAGCTTGCAGTTACCGATTGTACAGAAGCGATGCCAACCTTCATCTGT 63
 DB 145 ACCTACAGAACAGCTGCACT-GAGATGTGTGAGAACGCTTACCTGACCTGT 203
 QY 64 TGTATCTGAGATGAGCTGAGCTTCCAGAACGATCTGCTCCATCTACTATCAGTTGA 123
 DB 204 GGACATTGGAAACGCTATGAAAGCATTCGAAACGCTTACCTGACCTGAA 263
 QY 124 CACGGAGATCAGCCGTTGTCGCTTACGGAGACGCTGATCTGCTCCATCTACTATCAGTTGA 183
 DB 264 CATAGRACTA-ACGTGGCCGCCGCTAGCATGAGCTGAGCTGAGCTTACCTGACCTGCA 322
 QY 184 ACAAGGGCCCTCCCTCTACTGACCATGAGCTGAGCTGAGCTGAGCTGAGCTA 243
 DB 323 ACAAGGGATGCCAACACTAACACTAACACTAACACTAACACTAACACTAACACTGCA 382
 QY 244 ATTCATGCGGCCGCTAGCATGAGCCGAGCTGACCTGAGCTGAGCTGAGCTA 303
 DB 383 ACTTCCTGCTGCAGCCCTTGACCCGGAAAGGCCATGGAAAGCTCATTTGCTGTCA 442

PT Cancer
 XX Claim 1; Page 160-161; 189pp; English.
 XX }

CC The invention relates to an isolated polynucleotide comprising a sequence selected from 183 human DNA sequences (appearing as ABK70130-ABK70312), or their fragments, homologues, variants or complements and their encoded polypeptides. Also, included are an expression vector comprising the polynucleotide operably linked to an expression control sequence; a host cell transformed or transfected with an expression vector or; an isolated antibody, or its antigen-binding fragment that specifically binds to the polypeptide; a method for detecting the presence of a cancer in a patient; a fusion protein comprising at least the polypeptide; an oligonucleotide that hybridises to the polynucleotide under moderate stringent conditions; a method for stimulating and/or expanding T cells specific for a tumour protein; an isolated T cell population comprising T cells prepared from the method of above; a composition comprising a first component consisting of carriers and immunostimulants, and a second component selected from the polynucleotides, proteins, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide; methods for stimulating an immune response or treating cancer in a patient by administering the composition and diagnostic kits comprising at least one of the oligonucleotide of, or an antibody and a detection reagent consisting of a reporter group. The polypeptides and polynucleotides are useful as vaccines for the treatment or prevention of lung cancer, and for diagnosis and monitoring of such cancer. The polynucleotide, polypeptide and antigen presenting cells can be used to stimulate or expand T cells specific for a tumorous protein. The polynucleotides may be used as probes or primers for nucleic acid hybridisation, and in the preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The present sequence is one of the 183 lung cancer associated polynucleotides.

XX SQ Sequence 2247 BP; 591 A; 606 C; 612 G; 438 T; 0 other;

Query Match 76.9%; Score 318.4%; DB 24; Length 2247;
 Best Local Similarity 88.6%; Pred. No. 2.2e-95;
 Matches 365; Conservative 0; Mismatches 45; Indels 2; Gaps 2;

Qy 3 AACGTACAGAACAGCTTGCAAGTACCGATTGAGATGCAACCTTCATCTG 62
 Db 282 AACATACAGAACAGCCCTGCAAAATTA-CGATTTGTAACAAAGATCAACCTTCATCTG 340
 Qy 63 TTGATATCTGGATAATGATCGGAGTTCCGAGACATGGCTTACACGGTGGACACA 122
 Db 341 TTGATATCTGGACAGATTGAGCCCTTCAGACATGGCTTAAACATGGACATA 400
 Qy 123 GCACGGAGATCAGGCCCTGTCAGTACCGATGAGACCGTCACTCATCTACTATCAGTTG 182
 Qy 401 CCACCGAGATA-GTGTTGTCGCCCTCTACTACCAAAATPAGTGAACTCATCTACTATCAGTTG 459
 Qy 183 AACAAAGGCCCTCCCTCTACTACCAAGATCAGTCGCTGGTCCATCAGTCTCTACTC 242
 Db 460 AACAAAGGCCCTCCCTCTACTACCAAAATPAGTGAACTCATCTACTATCAGTTG 519
 Qy 243 AACATGTTGCGCCGCTTAAGACAGTGAGGCCGAGGCAAGCTTTCAGNT 302
 Db 520 AACATPATGATGCTGATAGACAGTGAGCTGGCCGGAGCTTTCAGTT 579
 Qy 303 AAAGCTATGTTAGCAACCATTGTTGTTGGAAAAAATCTGGACAAATTGAGATACTTTC 362
 Db 580 AAAGCTATGTTAGCAACCATTGTTGTTGGAAAAAATCTGGACAAATTGAGATACTTTC 639
 Qy 363 TCCCAATGTTAGATTCATGGCTTAATGTTGTTGAAAGCTTGACCAAGT 414
 Db 640 TCCCAATGTTAGATTCATGGCTTAATGTTGACCAAGT 691

AC AAS73627;
 XX DT 13-FEB-2002 (first entry)
 DE DNA encoding novel human diagnostic protein #9431.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 PD 11-OCT-2001.
 XX PP 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSEQ INC.)
 XX DR 2001-639362/73.
 DR P-PSDB; ABG09440.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
 XX PS Claim 1; SEQ ID NO 9431; 103pp; English.
 XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, PCR primers, oligomers, and for chromosome polymerase chain reaction (PCR), and gene mapping, and in recombinant production of (II). The sequence tags (II) are also used in diagnostics as expressed sequence tags (EST) to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 2518 BP; 717 A; 627 C; 588 G; 586 T; 0 other;
 Query Match 44.2%; Score 183; DB 23; Length 2518;
 Best Local Similarity 68.1%; Pred. No. 2e-52;
 Matches 280; Conservative 0; Mismatches 129; Indels 2; Gaps 2;
 Qy 4 ACGTACAGAACAGCTTGCAAGTTACCGATTGAGATGCAACCTTCATCTGTT 63
 Db 164 ACCTACAGAACAGATGCAAGCT-TAGTTGTTGACAAATGCAATTGACCTGGT 222
 Qy 64 TGATATCTGGATAATGATCGGAGACATGGCTTAAACAGCTGGACACAG 123
 Db 223 GGACATATGGATGTCATAGACAGTTGGCAAAATGCTGAAACCTGGACAAA 282
 RESULT 2
 AAS73627 ID AAS73627 standard; cDNA: 2518 BP.
 XX Db 283 CACTGACTCA-ACGTGTCGCCATTAGGCTGTGCTCAGTATTACAGCTCA 341

Diagnostic coding sequences of the invention.						
CC	Note: The sequence for this patent did not appear in the printed					
CC	specification, but was obtained in electronic formats directly from WIPO					
CC	at ftp wipo.int/pub/published...pct_sequences.					
XX						
SQ	Sequence 2520 BP; 714 A: 636 C; 598 G; 569 T; 3 other;					
	Query Match	4 13 88;	Score 181.4;	DB 23;	Length 2520;	
	Best Local Similarity	67.9%	Pred. No. 7.3e-52;			
	Matches	279;	Conservative	0;	Mismatches 130;	Indels 2;
						Gaps
QY	4	ACGTACGAAAGCTGTGCAAGTTACCGATTGTACAGAAACGATGCAACCTTCATCTGT	63			
Db	101	ACCTAGAAAGCATGCAACT-TAGGTTGTTCACAAAGAATGCAATTGACCTGGT	159			
QY	64	TGATATCGGATATGATCGAGCTTCCGGACAAATGGCTTAACCGTGGACCAAG	123			
Db	160	GGACATGGATGGATGAGCATAGAGCAATGGCAAATGGCTTAACCTGGACCAAA	219			
QY	124	ACGGAGTAGGGGTGAGACGGTCACTCTCCATCATATCAGTGA	183			
Db	220	CACTGACTCA-ACGTGTCGGCTAGAGGTGTGCTCTCCACTATTTTACAGCTCA	278			
QY	184	ACAAAGCCCTCTCCTACTACCAAGATCAGCGTGGAGCTCCATAGCTTCACTCA	243			
Db	279	ACAAAGGATGCCAACCACTACCAAAATCCATGTGGAGCTCCATGCCCTTTA	338			
QY	244	ATTATCGGTGGCGCTACAGCTAGGGCGAGCAGTGGCTGGAGCAGTTGAGCTTCA	303			
Db	339	ACTTCCTGGCTGGCGCTTGTGGCGTGGCTGGAGCTTGTGGAGCTTCA	398			
QY	304	AAGCTATTTGAGCAACCTATGTTGTTGAAATAATGCTGGACAAATTGAGATACTTCT	363			
Db	399	AAATGGCTTGTGCAATTGTGAGGGAGATGTGAGAAATTAGATAATTCT	458			
QY	364	CCCAATGGTGGATGTCGAAATGGCTTATGATGTTGGAAAGCTTGACAGT	414			
Db	459	CAATGATTTCTGACTCCAGTGGGTGATGGCTTATGGACGATATGACAAAT	509			
	RESULT	4				
	ABK70157					
	ID	ABK70157 standard; cDNA; 512 BP.				
	XX					
	AC	ABK70157;				
	XX					
	DT	15-JUL-2002. (first entry)				
	XX					
	DE	Human lung cancer associated cDNA DMSM-52.				
	XX					
	KW	Human; ss; gene; lung cancer; cytostatic; tumour; vaccine.				
	XX					
	OS	Homo sapiens.				
	XX					
	PN	WO200224057-A2.				
	XX					
	PD	28-MAR-2002.				
	XX					
	PF	20-SEP-2001; 2001WO-USA42232.				
	XX					
	PR	22-SEP-2000; 2000US-234837P.				
	PR	10-OCT-2000; 2000US-239440P.				
	PR	29-JUN-2001; 2001US-301928P.				
	XX					
	PA	(CORIXA CORP.				
	XX					
	PI	Benson DR, Mohamath R, Lodes MJ;				
	XX					
	DR	WPI; 2002-372001/40.				
	XX					
	PT	New tumour lung proteins and nucleic acids encoding the proteins, useful				
	PT	as vaccines and for treating, preventing, diagnosing or monitoring lung				
	PT	cancer				

XX Claim 1; Page 115; 189pp; English.

PS The invention relates to an isolated polynucleotide comprising a sequence selected from 183 human DNA sequences (appearing as ABK70130-ABK70312), or their fragments, homologues, variants or complements and their encoded polypeptides. Also included are an expression vector comprising the polynucleotide operably linked to an expression control sequence; a host cell transformed or transfected with an expression vector or; an isolated antibody, or its antigen-binding fragment that specifically binds to the polypeptide; a method for detecting the presence of a cancer in a patient; a fusion protein comprising at least the polypeptide; an oligonucleotide that hybridises to the polynucleotide under moderately stringent conditions; a method for stimulating a cell population comprising T cells specific for a tumour protein; an isolated T cell population comprising T cells prepared from the method of above; a composition comprising a first component consisting of carriers and immunostimulants, and a second component selected from the polynucleotides, proteins, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide; methods for stimulating an immune response or treating cancer in a patient by administering the composition and diagnostic kits comprising at least one of the oligonucleotide or, an antibody and a detection reagent consisting of a reporter group. The polypeptides and a polynucleotides are useful as vaccines for the treatment or prevention of lung cancer, and for diagnosis and monitoring of such cancer. The polynucleotide, polypeptide and antigen presenting cells can be used to stimulate or expand T cells specific for a tumorous protein. The polynucleotides may be used as probes or primers for nucleic acid hybridisation, and in the preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The present sequence is one of the 183 lung cancer associated polynucleotides.

XX Sequence 512 BP; 127 A; 135 C; 141 G; 109 T; 0 other;

XX Score 181; DB 24; Length 512;

XX Best Local Similarity 87.0%; Pred. No. 4e-52'; Length 3045;

XX Matches 221; Conservative 0; Mismatches 31; Indels 2; Gaps 2;

XX

Query Match 43.7%; Score 181; DB 24; Length 512;

XX Best Local Similarity 87.0%; Pred. No. 4e-52'; Length 3045;

XX Matches 221; Conservative 0; Mismatches 31; Indels 2; Gaps 1;

XX

Query	Match	Score	Length
3 AACGTACAGACAGCTTGGCAGTTACCGAATTCAGAGGATGCAACCTTCATCTTG	62	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
260 FACTAACAGACAGCTTGGCAGATTAA-CGATTGTACAAAGATGCAACCTTCATCTTG	318	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
63 TGTATATCTGAAATATGATCAAGTTTCGGAGAAATGGCTTAACCGTGGACACA	122	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
319 TGTATATCTGAAATGATCAAGTTTCGGAGAAATGGCTTAACCGTGGACACA	378	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
123 GCACGGAGATCAGGGCTGTNCGCCCTGGAGACCCTCATCTGCTCATATAGTTG	182	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
379 CCACCGAGATA- GTGTGTCCGCCCTGAACACTGTCATCTCCATCTACTATAGTTG	437	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
183 ACAAAAGCGCTTCCTCTACTACCAAGATCAGCGTGGAGCATCTCTCTACTC	242	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
438 ACAAGGGCCCTCCCTCTACTACCAAGATCAGCGTGGAGCATCTCTCTACTC	497	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
243 ATTTCATGGTGC	256	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
498 ACTTTATGATGTC	511	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;

XX

Query Match 36.4%; Score 150; DB 23; Length 3045;

XX Best Local Similarity 63.2%; Pred. No. 3.e-41; Mismatches 141; Indels 1; Gaps 1;

XX

Query	Match	Score	Length
29 CGATTGTACAGAAGCGATGCAACCTTCATCTGTTGATATCTGAAATATGATGCAACGCT	88	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
602 CGCTATATACAGAACTCACAATCTGACTTGGACATATGAAATGATGATGAGGCC	661	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
89 TTCCAGACATCTGGCTTAACACGTGGACACAGCAGAACGGCTGTNCGGCT	148	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
662 TTTCGGAGATGGCTTGAACACCTGGCTTGAAGGGAGGTTGA-GGGTGGCCAGGT	720	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
149 GGAGACCGTCATCTGGCTCATCTACTATGATGAAAGGGCTTCCTACTTCACCA	208	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
721 GGAACCTGGTCTCTCCCTATCATACCTAACAGGCTGCAACGGCTCAGCA	780	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
209 GATCAGCGTGGAGCAATCTACATCACTTCCTACTCAATTCATGTTGACGACAG	268	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
781 GGTGCTTGACTCGTCAACTGGGCTTGCTCAACTGGTGGCTGACACAG	840	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
269 TGAGGCCAGGGCTTACCGCTGTTTCAGTTAGGATGACCATGTTGCG	328	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
841 TGATAAACTGGGCAAGATACTGGCTTTCATCAAAGTGCCCTGGCCACTATGTC	900	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
329 TGGAAAATCTGGACAAATTGAGATACTTTCACATGTTGAGTCAATGGCT	388	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
901 TGGCAGCTGGTGGACAAACTAAGTCAGTTCTGGATCTGGATCTGGCT	960	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
389 AATGATGTTGGAAAGCTGACCT	414	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;
961 GCTGGCTGGCTGGAGCTGGCACT	986	3045	BP; 721 A; 882 C; 846 G; 596 T; 0 other;

XX

RESULT 5

ABL14199

ID ABL14199 standard; cDNA; 3045 BP.

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 37079.

KW Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical; gene; ss.

XX

ID	ABL14198	standard; cDNA; 15987 BP.
XX	AC	
XX	AC	
XX	XX	Drosophila melanogaster expressed polynucleotide SEQ ID NO 37076.
DE	XX	Drosophila; developmental biology; cell signalling; insecticide;
KW	XX	pharmaceutical; gene; ss.
KW	XX	Drosophila melanogaster.
OS	XX	
OS	OS	
XX	XX	
XX	PN	WO200171042-A2.
XX	XX	
XX	PD	27-SEP-2001.
XX	XX	
PF	PF	23-MAR-2001; 2001WO-US09231.
PF	PF	
P	P	13-MAR-2000; 2000US-191637P.
Ph	Ph	11-JUL-2000; 2000US-0614150.
XX	XX	
PA	PA	(PEKE) PE CORP NY.
XX	XX	
PI	PI	Venter JC, Adams M, Li PWD, Myers EW;
XX	XX	
DR	DR	WPI: 2001-654860/75.
DR	DR	
P-PSDB:	P-PSDB:	ABB70055.
XX	XX	
PT	PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
PT	PT	
PT	PT	
XX	XX	
PS	PS	Claim 1: SEQ ID NO 37076; 21pp + Sequence Listing; English.
XX	XX	
CC	CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (AAB857737-ABP74072).
CC	CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences .
CC	CC	
XX	XX	
SR	SR	Sequence 15987 BP: 4295 A; 3570 C; 3827 G; 4295 T; 0 other;
SR	SR	
every	Match	22.8%; Score 94.2; DB 23; Length 15987;
Best	Local Similarity	64.6%; Pred. No. 3.6e-21;
Matches	155; Conservative	0; Mismatches 84; Indels 1; Gaps
QY	QY	29 CGATTTGTACAGAAGCGATGCAACCTTACATCTTGTATATCTGGAAATATGATCGAAGCT 88
Ddb	455.8	CGCTATATAACAGAAGTCACAAATCTGCACCTTGTGACATATGGGACATATGGAAATGTGATCGAGGCC 4459
QY	QY	89 TTCGAGAACATGGCCTTAACCCCTGACCAAGACAGCAAGATGGCCTGTNNCGCT 148
Ddb	445.8	TTCGCGGAAATGGCCTGACACCTGGCCAGAGGAGGGA-GCTGGCAGGCT- GCTGGCAGGCT 4400
QY	QY	149 GGAGCCCTCATCTGTTCCATCTACTATGTTGACAAAGGCCCTCTCTACTTACCA 208
Ddb	439.9	GGAAACCTGGTCTCTCCCTCATTAACCTTAACAGGCCCTGACCTGAGCAG 4340
QY	QY	209 GATCAGCTGGAGCAGTCATCATGCTTCAATTICATGTCGCCGCTTACGACAG 268
Ddb	433.9	GGGCCCTGGACTCGAAAGGGGGTCTGCTGTCATGTCAGCTGTCATGACAG 4280

XX	AC	AAQ60778;
XX	XX	16-MAR-1994 (first entry)
XX	DT	
DE		Human brain Expressed Sequence Tag EST00891.
XX		Gene transcription product; genetic markers; tagging; <i>in vivo</i> ;
KW		transcription; mapping; locations; chromosomes; chromosomal; ss.
XX		
KW		
XX		
OS		Homo sapiens.
XX	XX	
PN	W09316178-A.	
XX	XX	
PD	19-AUG-1993.	
XX	XX	
PF	12-FEB-1993;	93WO-US01294.
XX	XX	
PR	12-FEB-1992;	92US-0837195.
XX	XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICE.	
XX	XX	
PI	Adams MD,	Moreno RF,
XX	DR	Venter CJ;
WPI	1993-272882/34.	
XX		
PT	Enriched oligonucleotides and corresp.	sequences - used as
PT	PT	markers for human genes transcribed <i>in-vivo</i> , facilitate tagging
PT	PT	of most human genes
XX	PS	Example 4: Page 388: 500pp; English.
XX	PS	
CC	The Expressed Sequence Tag was isolated from a human brain cDNA	
CC	library as part of a large set of ESTs which can be used as markers	
CC	for human genes transcribed <i>in vivo</i> . They can be used to facilitate	
CC	tagging of most human genes, for mapping locations of expressed genes	
CC	on chromosomes, for individual or forensic identification, for mapping	
CC	locations of disease-associated genes, for identification of tissue	
CC	type, and for prep. of antisense sequences, probes and constructs.	
CC	EST00891 has an "excellent" coding probability as evaluated using the	
CC	coding-region prediction program CRM. See also AAQ59041-0614440.	
XX	SO	Sequence 472 BP; 132 A; 100 C; 110 G; 120 T; 10 other;
Query	Match	19.7%
Best	Local	Score 81.4; DB 14; Length 472;
Similarity		Pred. No. 1..3e-17;
Matches	173; Conservative	Mismatches 83; Indels 6; Gaps
Qy	4	ACGTACAGAACAGCTTGCAGTTACCGATTGTCAGAAGGATGCAACCTTCATCTGT
Db	129	ACCTACGAAAGCATGCAACT-TAGGTGTTGTCAGAAGAATGCAATTGACCTGGT
Qy	64	TGATATCTGGAAATATGATCGAACAGCTTCAAGCAGAACAGCTTGAACGGTGGACCAAG
Db	188	GGACATATGGATGTCATAGAACATGGCGGAAATACTGCTGAAACACCTGGACCAA
Qy	124	CACGGGATCGGCTGTCGGCCTGAGACGCTCATCTGTCATCTGCTGCTGCTGCT
Db	248	CACTGACTCA-ACCTGTCGGCTGTCAGGGTGTGCTCTCCACTATTTTACCCAGCTC
Qy	183	AACAAAGCCCTTC -- -TTCTACTCACCAGATCAGGCTGGACGAGTCATCAGTCCTTA
Db	307	AACAAACGGGTGNCACACTTCACCAAAATCATGGAGCAGTCATCAGNCNTNCNTN
Qy	240	CTCAATTTCATGGTCCCGCT
Db	367	CTTAACTCTGCTTGGCAGCCT

RESULT 8
ABL87347/C
ID ABL87347 standard; CDNA; 689 BP.

DE Human diagnostic and therapeutic polynucleotide (DITHP) #157.

XX Human; receptor; diagnostic; therapeutic; gene therapy; vaccine; cell proliferative disorder; Crohn's disease; lymphoma; leukaemia; acquired immune deficiency syndrome; AIDS; autoimmune disorder; respiratory disorder; ss.

XX Homo sapiens.

PN WO200162927-A2.

XX 30-AUG-2001.

PD 21-FEB-2001; 2001IWO-US06059.

XX 24-FEB-2000; 2000US-0184693.

PR 24-FEB-2000; 2000US-0184697.

PR 24-FEB-2000; 2000US-0184698.

PR 24-FEB-2000; 2000US-0184768.

PR 24-FEB-2000; 2000US-0184769.

PR 24-FEB-2000; 2000US-0184770.

PR 24-FEB-2000; 2000US-0184771.

PR 24-FEB-2000; 2000US-0184772.

PR 24-FEB-2000; 2000US-0184773.

PR 24-FEB-2000; 2000US-0184774.

PR 24-FEB-2000; 2000US-0184776.

PR 24-FEB-2000; 2000US-0184777.

PR 24-FEB-2000; 2000US-0184813.

PR 24-FEB-2000; 2000US-0184837.

PR 24-FEB-2000; 2000US-0184841.

PR 24-FEB-2000; 2000US-0185213.

PR 24-FEB-2000; 2000US-0185216.

PR 12-MAY-2000; 2000US-0185285.

PR 15-MAY-2000; 2000US-0204226.

PR 16-MAY-2000; 2000US-0204221.

PR 16-MAY-2000; 2000US-0204221.

PR 16-MAY-2000; 2000US-0204908.

PR 17-MAY-2000; 2000US-0205232.

PR 17-MAY-2000; 2000US-0204615.

PR 17-MAY-2000; 2000US-0204863.

PR 17-MAY-2000; 2000US-0205221.

PR 17-MAY-2000; 2000US-0205285.

PR 17-MAY-2000; 2000US-0205286.

PR 17-MAY-2000; 2000US-0205287.

PR 17-MAY-2000; 2000US-0205223.

PR 17-MAY-2000; 2000US-0205324.

XY P. (INCY) INCYTE GENOMICS INC.

XX Panzer SR, Spiro PA, Banyville SC, Shah P, Chalup MS, Chang SC;

PI Chen A, D'Sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE;

PI Dufour GE, Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL;

PI Liu TF, Roseberry AM, Rosen BH, Russo FD, Stockdriener TK, Daffo A;

PI Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W;

PI Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;

XX DR 2001-502867/55.

DR P-PSDB; AAU19571.

XX PT Claim 1; Page 370-371; 522pp; English.

XX PT The invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DITHP) polypeptides (II), which include e.g. enzymes,

CC and proteins involved in growth and development and receptors. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate DITHP expression. For example, (I) and (II) may be used to treat disorders associated with decreased polypeptide

CC expression by rectifying mutations or deletions in a patient's genome;

XX PT Improved gene therapy with phage vectors unable to release genetic

CC samples, and therefore which patients may be in need of restorative

CC therapy. (II) may also be used as antigens in the production of

CC antibodies against DITHPs and in assays to identify modulators of DITHP

CC expression and activity. The anti-DITHP antibodies and antagonists may

CC also be used to down regulate expression and activity. The anti-DITHP

CC antibodies may also be used as diagnostic agents for detecting the

CC presence of DITHPs in samples (e.g., by enzyme linked immunosorbent

CC assay (ELISA)). AAS30986-AAS31196 represent human diagnostic and

CC therapeutic (DITHP) polynucleotides of the invention.

XX SQ Sequence 5106 BP; 1248 A; 1387 C; 1268 G; 1203 T; 0 other;

XX Query Match 9 5%; Score 39.2; DB 22; Length 5106;

CC Best Local Similarity 51.1%; Pred. No. 0.022;

CC Matches 89; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

XX Qy 206 CCAGATCAGCGGTGGAGTCATAGTCCTACTCAATTCACTGTCCTAGCTTACAGA 265

CC Db 1711 CCTGGTCATGTCGACTCTGTCGACATGCTGTTAGCTTACATGTTGTTG 1770

CC Qy 266 CAGTGGGGCGGAGGGCAGGGTGAAGCTATGTTAGCAACCATGTTG 325

CC Db 1771 TAGTGGTCAGTCGAAAGATGGGGCATGTGCTTTAGACTGGCATGTCATG 1830

CC Qy 326 TGGCGAAAGAATGCTGGAGAATGAGATGCTCCAGATGTCAGATTC 379

CC Db 1831 TGGCACGGGAGTGAGGGAAAACCTCAGTACCTCTTCAGCCAAGTGCCAACTC 1884

RESULT 1.1

AAV18885

ID AAV18885 standard; cDNA: 13815 BP.

XX XX

AC AAV18885;

XX XX

DT 17-AUG-1998 (first entry)

XX XX

DE Mus musculus dystrophin cDNA.

XX XX

PCR primer; phage vector; bacteriophage lambda; gene therapy;

XX KW antisense RNA; ribozyme; delivery; vaccine; antigen; treatment;

XX KW prevention; in vivo; in vitro; AIDS; cancer; cystic fibrosis;

XX KW acquired immune deficiency syndrome; Gaucher's disease; haemophilia;

XX KW post-translational modification; diagnostic reagents; production;

XX KW dystrophin; ss.

XX OS Mus musculus.

XX PN WO9805344-A1.

XX XX

PR 12-FEB-1998.

XX XX

PR 03-JUL-1997; 97WO-US12928.

XX XX

(BGHM) BRIGHAM & WOMENS HOSPITAL

XX XX

Dubin DB, Kupper TS, Sarkar SN;

XX DR WPI; 1998-145345/13.

XX XX

Improved gene therapy with phage vectors unable to release genetic

Query Match 9.2%; Score 38.2; DB 24; Length 13815;
 Best Local Similarity 53.0%; Pred. No. 0.085; Indels 0; Gaps 0;
 Matches 79; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 240 CTCAAATTCATGTCGCGCTTCAGACTGGGGCAGGTGACAGTGGCCGAGCTGTTCA 299
 Db 9734 CTCAACTGGCTTCATGTTATGATACGGGACGAAACGGGAGATCCGTGTCCTGCT 9793
 Qy 300 GNTAAAGCTATGTTAGCACCAGTGTGGAAATATGCTGGACAAATGGAGATACATT 359
 Db 9794 TTTAAAATGGCATCATTCCTGTGAAAGGACACTTGGAGACAGTACAGATACCTT 9853
 Qy 360 TCTCCCAAGATGTCAGATCCATGGCT 388
 Db 9854 TCAAGCAAGTGGCAAGTTCAGTGGCTT 9882

RESULT 14
 AAT~2558/C
 VAT2558 standard; cDNA; 19307 BP.

X:
 AC AAT27558;

DT 07-AUG-1996 (first entry)

XX Shuttle vector pAdEl.CMVdys.

XX Adenovirus type 5; Ad5; vector; gene therapy; gene transfer;

XX helper virus; dystrophin; muscular dystrophy; ds; cyclic.

OS Synthetic.

PN W09613597-A2.

XX 09-MAY-1996.

XX 27-OCT-1995; 95WO-US14017.

XX 28-OCT-1994; 94US-03313881.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX Chen S, Fisher KJ, Weitzman M, Wilson JM;

PI DR; 1996-251463/25.

XX Recombinant adenovirus produced from shuttle vector and helper virus

PT - has crippled packaging function, useful for delivering
 P. transgene(s) to target cells

PS Example 9; Fig 12A-12P; 149pp; English.

XX Shuttle vector pAdEl.CMVdys (AAT27558) comprises the adenovirus
 CC elements needed for replication and virion encapsidation but
 CC is deleted of all viral genes. It carries a mouse dystrophin
 CC minigene under control of the CMV promoter. It is used with a helper
 CC virus that supplies the sequences needed for a productive viral
 CC infection but which has disabled packaging function. Recombinant
 CC adenovirus is produced that is characterized by high titer transgene
 CC delivery to host cells and the ability to stably integrate the
 CC transgene into the host cell chromosome. Such a vector can be used
 CC to transfer the dystrophin gene for use in muscular dystrophy gene
 XX therapy.

Sequence 19307 BP; 4816 A; 4393 C; 4056 G; 6042 T; 0 other;

Query Match 9.2%; Score 38.2; DB 17; Length 19307;
 Best Local Similarity 53.0%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;

Qy 240 CTCATTTATGGTGGCCGCTACGACAGTGAAGGCGAGGCAAGTGGCTTCA 299
 Db 4951 CTCAACTGGCTTCATGTTATGATACGGGAGAACGGGAGATCGTGCCTGTC 4892

Query Match 9.2%; Score 38.2; DB 17; Length 19307;
 Best Local Similarity 53.0%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX

Qy 300 GNTAAAGCTATGTTAGCACCAGTGTGGAAATATGCTGGACAAATGGAGATACATT 359
 Db 4891 TTAACTGGATCATTCATGTTGAAGACATTTGGAGACAGTACAGATACCTT 4832

Qy 360 TTCTCCCAAGATGTCAGATCCAAATGGCT 388
 Db 4831 TCAAGCAAGTGGCAACTCAACTGGCT 4803

RESULT 15
 ABK81993
 ID ABK81993 standard; DNA; 887 BP.

XX
 AC ABK81993;
 XX
 DT 13-AUG-2002 (first entry)
 XX Human dystrophin C-terminal polynucleotide.

XX Mini-dystrophin peptide; spectrin-like repeat domain; muscle disease;
 KW Duchenne's muscular dystrophy; DMD; dystrophin; human; ds.
 XX
 Homo sapiens.
 XX
 PN WO200229056-A2.
 XX
 PA WO200229056-A2.
 PD 11-APR-2002.
 XX
 PR 04-OCT-2001; 2001WO-US31126.
 XX
 PR 06-OCT-2000; 2000US-238848P.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Chamberlain JS, Harper SQ.
 XX
 DR WPI; 2002-435334/46.
 XX
 PT A composition for preparing therapeutic drugs, has a mini-dystrophin
 PT peptide comprising a specific number of spectrin-like repeat domains,
 PT or a nucleic acid sequence encoding the mini-dystrophin peptide
 XX Disclosure; Fig 9; 145pp; English.

XX The invention describes a composition comprising a mini-dystrophin
 CC peptide comprising a spectrin-like repeat domain, where the domain
 CC comprises n spectrin-like repeats, and contains no more than n
 CC spectrin-like repeats, where n is an even number between 4-24, or a
 CC nucleic acid encoding a mini-dystrophin peptide. The mini-dystrophin
 CC peptide or the polynucleotide encoding it is useful as a medicament,
 CC for preparing a drug for therapeutic application and in the preparation
 CC of a composition for treatment of muscle disease, e.g. Duchenne's
 CC muscular dystrophy (DMD). This sequence represents a human dystrophin
 CC polynucleotide sequence used in the creation of the mini-dystrophin
 CC peptides of the invention.

Sequence 887 BP; 244 A; 207 C; 213 G; 223 T; 0 other;

Query Match 9.0%; Score 37.2; DB 24; Length 887;
 Best Local Similarity 50.0%; Pred. No. 0.039; Mismatches 90; Indels 0; Gaps 0;

Qy 209 GATCAGCGTGGAGTCATCAGTCCTACTCAATTCATGGTTCGGCCCTACGACAG 268
 Db 168 GGTCACGCGCCCTCTGGCTGGATATGGTCTGACTGCTGTTATGATAC 227

Qy 269 TGGGGCCGAGGCCGANGTTGACCTTAAGGTATGGTTAGCAACCAGTGTGG 328
 Db 228 GGGACAAAGGGGATCGTCTGCTTAAAATGGCATTCATCCTCCGGTGPAA 287

Qy 329 TGGAAAATGGTGGACAAATTGAGATTCACATTGGTCAATGGCTGCTGTC 388
 Db

Db 288 AGCACATTGGAAAGACAAAGTACAGATAACCTTTCAAGCAAGTGGCAAGTCAACAGGATT 347

Search completed: December 1, 2002, 16:24:34
Job time : 290 secs

Run on: OM nucleic - nucleic search, using sw model

Page 1

Title: Perfect score: Sequence: Scoring table: Sequence-derived:

US-09-680-959-125 414 1 ctaacgtacagaaacagcttg. gttngaaagctgaccagt 414

TO, number of hits satisfying chosen parameters:

341543 seqs, 192557720 residues

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Database : Publishing_Applications

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4: /cgn2_6/ptodata/2/pubpna/us07_pubcomb_seq:*

5: /cgn2_6/ptodata/2/pubpna/us06_pub_seq:*

6: /cgn2_6/ptodata/2/pubpna/us06_pubcomb_seq:*

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11: /cgn2_6/ptodata/2/pubpna/us09_pub_seq:*

12: /cgn2_6/ptodata/2/pubpna/us10_pub_seq:*

13: /cgn2_6/ptodata/2/pubpna/us10_pubcomb_seq:*

14: /cgn2_6/ptodata/2/pubpna/us60_pub_seq:*

Pred. No. is the number of results predicted by analysis of the total score distribution being printed, and is derived by analysis of the total score distribution being printed.

result No. Score

1 318.4 76.9 2247 10 US-09-960-253-157

Query Match Length DB ID

2 181 43.7 512 10 US-09-960-253-157

Description

3 78.4 18.9 689 10 US-09-960-253-157

Sequence 157, App

4 37.2 9.0 13957 10 US-09-960-253-157

Sequence 28, App

5 37.2 9.0 13957 10 US-09-960-253-157

Sequence 22, A

6 32.2 7.8 1173 9 US-09-960-253-157

Sequence 10125, A

7 32.2 7.8 1173 9 US-09-960-253-157

Sequence 2284, App

8 30.8 7.4 1040 10 US-09-938-8424-1992

Sequence 1992, App

9 29.6 7.2 1098 9 US-09-88-546-3

Sequence 1, App

10 29.6 7.1 1927 10 US-09-88-546-3

Sequence 3, App

11 29.6 7.1 1927 9 US-09-815-242-7522

Sequence 7522, App

12 29.6 7.1 2734 9 US-09-764-868-66

Sequence 66, App

13 29.2 7.1 2964 10 US-09-198-559-2

Sequence 489, App

14 29.2 7.1 307 10 US-09-294-09-B-1641

Sequence 2, App

15 29.2 7.1 348 10 US-09-864-761-21541

Sequence 1641, App

16 28.8 7.1 442 10 US-09-864-761-21541

Sequence 2156, App

17 28.6 6.9 357 10 US-09-887-576-408

Sequence 4808, App

18 28.6 6.9 402 10 US-09-877-564-462

Sequence 301, App

19 28.6 6.9 408 10 US-09-878-574-4089

Sequence 4089, App

20 28.6 6.9 4089 10 US-09-878-574-4089

Sequence 4809, App

21 28.6 6.9 4090 10 US-09-878-574-4089

Sequence 4810, App

22 28.6 6.9 4091 10 US-09-878-574-4089

Sequence 4811, App

23 28.6 6.9 4092 10 US-09-878-574-4089

Sequence 4812, App

24 28.6 6.9 4093 10 US-09-878-574-4089

Sequence 4814, App

25 28.6 6.9 4094 10 US-09-878-574-4089

Sequence 4815, App

26 28.6 6.9 4095 10 US-09-878-574-4089

Sequence 4816, App

27 28.6 6.9 4096 10 US-09-878-574-4089

Sequence 4817, App

28 28.6 6.9 4097 10 US-09-878-574-4089

Sequence 4818, App

29 28.6 6.9 4098 10 US-09-878-574-4089

Sequence 4819, App

30 28.6 6.9 4099 10 US-09-878-574-4089

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31 28.6 6.9 4100 10 US-09-878-574-4089

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32 28.6 6.9 4101 10 US-09-878-574-4089

Sequence 4822, App

33 28.6 6.9 4102 10 US-09-878-574-4089

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34 28.6 6.9 4103 10 US-09-878-574-4089

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35 28.6 6.9 4104 10 US-09-878-574-4089

Sequence 4825, App

36 28.6 6.9 4105 10 US-09-878-574-4089

Sequence 4826, App

37 28.6 6.9 4106 10 US-09-878-574-4089

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38 28.6 6.9 4107 10 US-09-878-574-4089

Sequence 4828, App

39 28.6 6.9 4108 10 US-09-878-574-4089

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40 28.6 6.9 4109 10 US-09-878-574-4089

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41 28.6 6.9 4110 10 US-09-878-574-4089

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42 28.6 6.9 4111 10 US-09-878-574-4089

Sequence 4832, App

43 28.6 6.9 4112 10 US-09-878-574-4089

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44 28.6 6.9 4113 10 US-09-878-574-4089

Sequence 4834, App

45 28.6 6.9 4114 10 US-09-878-574-4089

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46 28.6 6.9 4115 10 US-09-878-574-4089

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47 28.6 6.9 4116 10 US-09-878-574-4089

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Sequence 4839, App

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51 28.6 6.9 4120 10 US-09-878-574-4089

Sequence 4841, App

52 28.6 6.9 4121 10 US-09-878-574-4089

Sequence 4842, App

53 28.6 6.9 4122 10 US-09-878-574-4089

Sequence 4843, App

54 28.6 6.9 4123 10 US-09-878-574-4089

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55 28.6 6.9 4124 10 US-09-878-574-4089

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58 28.6 6.9 4127 10 US-09-878-574-4089

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59 28.6 6.9 4128 10 US-09-878-574-4089

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61 28.6 6.9 4130 10 US-09-878-574-4089

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97 28.6 6.9 4166 10 US-09-878-574-4089

Sequence 4887, App

98 28.6 6.9 4167 10 US-09-878-574-4089

FILE REFERENCE: 44921-5028-WO
 CURRENT APPLICATION NUMBER: US/09/880,107
 CURRENT FILING DATE: 2001-06-14
 PRIOR APPLICATION NUMBER: US 60/211,379
 PRIOR FILING DATE: 2000-06-14
 PRIOR APPLICATION NUMBER: US 60/237,054
 PRIOR FILING DATE: 2000-10-02
 NUMBER OF SEQ ID NOS: 3950
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2284
 LENGTH: 13957
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Genbank Accession No. US20020142981A1 M18533

Query Match 9.0%; Score 37.2; DB 10; Length 13957;
 F:t Local Similarity 50.0%; Pred. No. 0.05; DB 90; Mismatches 0; Indels 0; Gaps 0;
 :thes 90; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 209 GATCAGCTGGACAGTCATAGTCCTACTCAATTCAATTCATGTCGGCTACGAG 268
 Db 9712 GTCACAGTCCCTCTCGTGGATATGTTGATGTTGATGTTGATGATA 9771

Qy 269 TAGGGCCGAGGGCAGNTGACCGTGTTCAGNTAAAGCTTGTAGCAACCATGTTGG 328
 Db 9772 GGAGAGACAGGAGGATCCGGTCCGTCGTCATTTAAACTGCATTCCTGCTAA 9831

Qy 329 TGGAAAAATGGCTGGACAAATTGAGATACATTTCTCCAGATGTCAGATTCCAAATGGCTT 388
 Db 9832 AGCACATTGGAGAACAGTACAGATACCTTTCAGCAAGTGGCAAGTTAACAGGATT 9891

RESULT 6
 US-09-938-842A-1992/C
 Sequence 1992, Application US/09938842A
 GENERAL INFORMATION:
 APPLICANT: Harper, Jeff
 APPLICANT: Kreps, Joe L
 APPLICANT: Wang, Xun
 APPLICANT: Zhu, Tong
 TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 FILE REFERENCE: SCRI1300-3
 CURRENT APPLICATION NUMBER: US/09/938, 842A
 CURRENT FILING DATE: 2001-08-24
 PRIOR APPLICATION NUMBER: US 60/227, 866
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: US 60/264, 647
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/300, 111
 PRIOR FILING DATE: 2001-06-22
 NUMBER OF SEQ ID NOS: 5379
 LENGTH: 1173
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1992

Query Match 7.8%; Score 32.2; DB 9; Length 1173;
 Best Local Similarity 47.9%; Pred. No. 0.57; DB 91; Mismatches 99; Indels 0; Gaps 0;

Qy 15 AGCTTGCAAGTACCGATTGTACAGAACCTTCATCTGTGATATCTGGA 74
 Db 206 ACTTCTAAAGTCCCGTGAAGCCAGGAGATCGCAAAGCTCTTGGAGAGAGA 147

Qy 75 ATATGATCGAAGCTTTCGAAATAACAGCTTGGACACAGAGATCA 134
 Db 146 ATAGGATAGTATAATATGAGACGCGTGGCATGATGATGAGATCAGGGAAAGT 87

RESULT 7
 US-09-825-345-1/C
 Sequence 1, Application US/09825345
 Patent No. US20020106750A1
 GENERAL INFORMATION:
 APPLICANT: FARWICK, MIKE
 APPLICANT: HUTHMACHER, KLAUS
 APPLICANT: BREHME, JENNIFER
 APPLICANT: PFEFFERLE, WALTER
 TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES WHICH CODE FOR THE def GENE
 FILE REFERENCE: 21123/280107/MAS
 CURRENT APPLICATION NUMBER: US/09/825, 345
 CURRENT FILING DATE: 2001-04-04
 PRIOR APPLICATION NUMBER: DE 100 46 228.6
 PRIOR FILING DATE: 2000-09-19
 PRIOR APPLICATION NUMBER: DE 101 13 957.8
 PRIOR FILING DATE: 2001-03-22
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 1040
 TYPE: DNA
 ORGANISM: Corynebacterium glutamicum
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (254)..(832)
 OTHER INFORMATION: def gene
 US-09-825-345-1

Query Match 7.7%; Score 32; DB 10; Length 1040;
 Best Local Similarity 60.2%; Pred. No. 0.63;
 Matches 53; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 49 CAACCTCTCATCTGTGATATCTGGAAATATGTCGAAAGCTTCGAGACATGGCTTAA 108
 Db 374 CATCCATCGTCGTCGATATCTGCAATAGTCGAACTTCCTGCAAGTCAGACATCCTCAGTAA 315

Qy 109 CACGCTGGACCAACGGACGGAGATCAG 136
 Db 314 CAAGCTGGTAGGGTTGGGAAACAGG 287

RESULT 8
 US-09-858-546-3
 Sequence 3, Application US/09858546
 Patent No. US20020172995A1
 GENERAL INFORMATION:
 APPLICANT: SHAO, Wei et al
 TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, AND
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
 FILE REFERENCE: CL001232
 CURRENT APPLICATION NUMBER: US/09/858, 546
 CURRENT FILING DATE: 2001-05-17
 NUMBER OF SEQ ID NOS: 5
 SEQ ID NO 3
 LENGTH: 80959
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(80959)
 OTHER INFORMATION: n = A,T,C or G

Patent No. US20020025930A1
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Corley, Neil C.
 APPLICANT: Shah, Purvi
 TITLE OF INVENTION: RAS-LIKE PROTEIN
 NUMBER OF SEQUENCES: 3
 ADDRESSEE: Inoyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/198,559
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/846,790
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REFERENCE/DOCKET NUMBER: 36-749
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2964 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: COUNTRY16
 CLONE: 2791521
 US-09-198-559-2

Query Match
 Best Local Similarity 7.1%; Score 29.6; DB 10; Length 2964;
 -ches 62; Conservative 53%; Pred. No. 7.9; Indels 0; Gaps 0;

Qy 58 TCTTGTGATATGATCGAACGTTCCGAGAAATGGCTTAACACGCTGGA 117
 Db 863 TCTCTTCATATACGAAAGGGCAAGGTTGGCTCATACGGAGATACTGGG 804

Qy 118 CCACACGAGGAGATCAGGGTGTCCGGCTCATCTCGTCCATCTACT 174
 Db 803 TCCCTATGAGGACATAAGGACGTGAGCTGGCATGAGCTGGGACCCATT 747

RESULT 13
 US-09-294-093B-1641
 Sequence 1641, Application US/09294093B
 GENERAL INFORMATION:
 APPLICANT: Talagdi, Raghunath, V.
 APPLICANT: Ito, Laura, Y.
 APPLICANT: Sherman, Bradley, K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
 FILE REFERENCE: PL-0009 US
 CURRENT APPLICATION NUMBER: US/09/294,093B
 CURRENT FILING DATE: 1999-04-16
 PRIOR APPLICATION NUMBER: 60-082,567
 PRIOR FILING DATE: April 21, 1998
 NUMBER OF SEQ ID NOS: 6207

SOFTWARE: PERL Program
 SEQ ID NO 1641
 LENGTH: 307
 TYPE: DNA
 ORGANISM: Zea mays
 NAME/KEY: misc feature
 OTHER INFORMATION: Inoyte ID NO. US20010051335A1 70034740H1
 NAME/KEY: unsure
 LOCATION: 12-13, 30-31, 41, 43-44, 70, 79, 81, 105-106, 140, 153, 178, 192, 196, US-09-294-093B-1641
 OTHER INFORMATION: a, t, c, g, or other

Query Match
 Best Local Similarity 7.1%; Score 29.2; DB 10; Length 307;
 -ches 58; Conservative 51.8%; Pred. No. 2.7; Indels 0; Gaps 0;

Qy 139 TGTNCGGCCTGGAGACGGCATCTCTGTCATCTACTATCAGTTGACAAGGCCPTCCCT 198
 Db 146 TATATCANGTTCAGGGAGAGAGTCATCCTCTATAAGGGCTNAAANTGGCTCCCTG 205

Qy 199 CTACTCACAGATCACGGTGGAGCATGTCCTACTCAATTATCAT 250
 Db 206 CGATTAACGAGTTCACCCAGGCTGGACGCCAAGCGTATNCAGCTGCT 257

RESULT 14
 US-09-864-761-21546/C
 Sequence 21546, Application US/09864761
 Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY
 FILE REFERENCE: Aeomica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,293
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 21546
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL009181.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2
; OTHER INFORMATION: EST HUMAN HIT: BE252309.1, EVALUATE 2.10e-02
; OTHER INFORMATION: NT HIT: 911156112, EVALUATE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P41143, EVALUATE 6.00e-48
; US-09-864-761-21546

Query Match Score 7.1%; Score 29.2%; DB 10; Length 348;
Best Local Similarity 48.7%; Pred. No. 2.9; Indels 0; Gaps 0;
Matches 76; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

Qy 135 GCGGTGTNCCGCTGGAGACCGTCATCTGCCATGACTATCAGTTGAAAGGGCCTT 194
Db 182 GCGAGCTGCTGCAGGGCTGCTCCATGCACTACAATATGTCACCCAGCATC 123

Qy 195 CCTCTACTCACCAGTACGGTGGACAGTCATAGTCCTACTCAATTCTATGGTC 254
Db 122 TTCACGCTCACCATGAGTGTGGCTACATGCTGTCACCCCTGTCAAGGCC 63

Qy 255 GCGCCTACGACGATGAGGGCGAGGTGACCC 290
Db 62 CTGGACTTCGACGCTGCCAAGGCCAAGTGATC 27

RESULT 15
; Sequence 4808, Application US/09864761
; Patent No. US2002008765A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864-761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

Query Match Score 7.1%; Score 29.2%; DB 10; Length 442;
Best Local Similarity 48.7%; Pred. No. 3.4; Indels 0; Gaps 0;

Qy 135 GGCGTGTNCCGCTGGAGACCGTCATCTGCCATGACTATCAGTTGAAAGGGCCTT 194
Db 417 GGCGACTGTGCTGCAAGGGTGTCTCCACTACATAATGTCACCCAGCATC 358

Qy 195 CCTCTACTCACCAGTACGGTGGACAGTCATAGTCCTACTCAATTCTATGGTC 254
Db 357 TTACAGCTACCATGATGAGTGTGACCCCTGTCACCCAGCTGTCAAAGGCC 298

Qy 255 GCGCCTACGACGATGAGGGCGAGGTGACCC 290
Db 297 CTGGACTTCGGACGCCCTGCCAAGGCCAAGCTGATC 262

Search completed: December 1, 2002, 17:45:07
Job time : 91 secs

availability will be considered under appropriate and limited collaborative arrangements.

Seq primer: M13 Reverse.

Location/Qualifiers

1. .505

/organism="Mus musculus"

/db_xref="NC_000910"

/clone_id="M_NH_BMAP_M_S4"

/dev_stage="27-32 days"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pT7D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The

NIH_BMAP_M_S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S4, NIH_BMAP_M_S3_3, NIH_BMAP_M_S3_2, NIH_BMAP_M_S3_1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S4) was constructed as follows: PCR-amplified cDNA inserts from NIH_BMAP_M_S3_3, NIH_BMAP_M_S3_2, and NIH_BMAP_M_S3_1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3_3, NIH_BMAP_M_S3_2, and NIH_BMAP_M_S3_1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-805, 1996)"

BASE COUNT 134 a 113 c 128 g 130 t

ORIGIN

Query Match 92.4%; Score 382.4; DB 10; Length 505;
Best Local Similarity 98.3%; Pred. No. 1.8e-107; Mismatches 405; Conservative 0; Indels 5; Gaps 2;

Db 498 AACGTACAGACAGCTTGTGAAAGTTAACCGATTGTACAGAAGGGATGCAACCTTCATCTTG 62

Db 63 TGTATATCGGAAATATGATGAGGTTCCGAGAACATGGCCTTAACAGGTGGACCA 122

Db 439 TGTATATCGGAAATATGATGAGGTTCCGAGAACATGGCCTTAACAGGTGGACCA 380

Db 123 GCACGGAGATCAAGGGGTGTCGGCTGGACCCGCAATCTGTCATCTACTATCAGTGT 182

Db 379 GCACGGAGATCA-GGGTGTCCGGCTGGACCCGTCATCTGTCATCTACTATCAGTGT 321

Db 183 ACAAGGCCTTCCCTCTACTACAGAGATCAACCTGGAGCAAGCTCTACTC 242

Db 320 ACACAGGCCTTCCCTCTACTACAGAGATCAACCTGGAGCAAGCTCTACTC 261

Db 243 ATTTCATGGTGCCTGAGCTGAGCTGAGGCGGAGGCAAGTTTCATCTTG 302

Db 260 ATTTCATGGTGCCTGAGCTGAGGCGGAGGCAAGTTTCATCTTG 201

Db 303 AAAGCTATGTTAGACCAATGTTGTTGGAAATAATGGATACATTTC 362

Db 200 AAAGCTATGTTAGCCTACATGTTGCTGGAAATAATGGATACATTTC 141

Db 363 TCCCAAGATGTCAGATCCAAATGGCTTAATGTTGTTGGAAAGCTGACAGT 414

Db 140 TCCCAAGATGTCAGATCCAAATGGCTTAATGTTGAAAGCTGACAGT 89

RESULT 2 AI3255959 517 bp mRNA linear EST 23-DEC-1998
LOCUS mq63d07.x1 Soares-thymus_2NbMT Mus musculus cDNA clone IMAGE:583405
DEFINITION 3' similar to TR:Q13197 Q13197 DYSTROREVIN-DELTA. [1] ; mRNA
SEQUENCE AI3255959
ACCESSION • EST. GI:4060388
KEYWORDS • house mouse.
ORGANISM Mus musculus
SOURCE house mouse.
REFERENCE 1 (bases 1 to 517)
AUTHORS Maria M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geise,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and Watson,R.
TITLE The WashU-HMMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:354053
This clone was previously sequenced on the 5' end only, this new data is from the 3' end
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 463.
Location/Qualifiers
1. .517
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:583405"
/clone_lib="Soares_thymus_2NbMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="A week"
/lab_host="DH10B"
/note="Vector: pT7D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5', TGTATACATCGAAAGTGGAGGGCCGTTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 139 a 126 c 129 g 123 t
ORIGIN
Query Match 87.7%; Score 363; DB 9; Length 517;
Best Local Similarity 98.7%; Pred. No. 1.9e-101; Mismatches 3; Indels 2; Gaps 2;
Matches 385; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
Qy 3 AACGTACAGACAGCTTGTGAAAGTTAACCGATTGCAAGTTGGCAACCTTCATCTTG 62
Db 498 AACGTACAGACAGCTTCCAGTTAGCTGTTACAGAGCTGCAACCTTCATCTTG 440
Db 63 TGTATATCGGAAATATGATGAGGTTCCGAGAACATGGCCTTAACAGGTGGACCA 122
Db 439 TGTATATCGGAAATATGATGAGGTTCCGAGAACATGGCCTTAACAGGTGGACCA 380
Qy 123 GCACGGAGATCAAGGGGTGTCGGCTGGACCCGCAATCTGTCATCTACTATCAGTGT 182
Db 379 GCACGGAGATCA-GGGTGTCCGGCTGGACCCGTCATCTGTCATCTACTATCAGTGT 321
Qy 183 ACAAGGCCTTCCCTCTACTACAGAGATCAACCTGGAGCAAGCTCTACTC 242
Db 320 ACACAGGCCTTCCCTCTACTACAGAGATCAACCTGGAGCAAGCTCTACTC 261
Qy 243 ATTTCATGGTGCCTGAGCTGAGCTGAGGCGGAGGCAAGTTTCATCTTG 302
Db 260 ATTTCATGGTGCCTGAGCTGAGGCGGAGGCAAGTTTCATCTTG 201
Qy 303 AAAGCTATGTTAGACCAATGTTGTTGGAAATAATGGATACATTTC 362
Db 200 AAAGCTATGTTAGCCTACATGTTGCTGGAAATAATGGATACATTTC 141
Qy 363 TCCCAAGATGTCAGATCCAAATGGCTTAATGTTGTTGGAAAGCTGACAGT 414
Db 140 TCCCAAGATGTCAGATCCAAATGGCTTAATGTTGAAAGCTGACAGT 89
Qy 123 GCACGGAGATCAGGGTGTGTCGGCTGTNNCCGGCTGGAGACCCGTCATCTGTCATCTACTATCAGTGT 182

Db 249 GCACGGAGATCA-GCGTGTCCGCTGGAGACGGTCATCTCGTCCATCTACTATCAGTTG 307
 Qy 183 AACAGGGCCTTCCTTCACTACCAGATCAGGGCAGCACTCCATCTACT 242
 Db 308 AACAGGGCCTTCCTTCACTACCAGATCAGGGCAGCACTCCATCTACT 367
 Qy 243 AATTTCATGGTCGCCGCTTACGACAGTGGGGCCGAGGCANGTGACCGTGTTCAGNT 302
 Db 368 AATTTCATGGTCGCCGCTTACGACAGTGGGGCCGAGGCANGTGACCGTGTTCAGNT 427
 Qy 303 AAGCTATGTTGACCAACATGGTGGGAAATAATGCTGAGAAATTGAGATACATTTC 362
 Db 428 AAGCTATGTTGACCAACATGGTGGGAAATAATGCTGGACAAATTGAGATACATTTC 487
 Qy 363 TCCCAGAATGTCAGATCCAAATGGCTTAAATG 392
 Db 488 TCCCAGAATGTCAGATCCAAATGGCTTAAATG 517

R_3
 BG865074
 Locus BG865074 958 bp mRNA linear EST 29-MAY-2001
 Definition 602784226f1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4910166',
 mRNA sequence.
 Accession BG865074
 Version 1
 GI:14215612
 Keywords EST.
 Source house mouse.
 Organism Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Reference NIH-NCGC http://mgc.nci.nih.gov/./
 Authors National Institutes of Health, Mammalian Gene Collection (MGC)
 Title Unpublished (1999)
 Comment Contact: Robert Strausberg, Ph.D.
 Email: cgsbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The T.M.A.G.E. Consortium (TLLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the T.M.A.G.E. Consortium/TLLN at:
 http://image.llnl.gov
 Plate: LLNL0810 row: d column: 07
 High quality sequence stop: 734.
 Location/Qualifiers
 1.. 958
 'RES
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 /strain="FVB/N"
 /db_xref="taxon:10050"
 /clone="IMAGE:4910166"
 /clone_lib="NCI_CGAP_SG2"
 /lab_host="DH10 (T1 phage-resistant)"
 /note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
 NotI; Site_2: SalI; Loned unidirectionally. Primer: Oligo
 DT. Average insert size 1.3 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 247 a 264 c 235 g 212 t
 ORIGIN
 Query Match 84.1%; Score 348.2; DB 12; Length 958;
 Best Local Similarity 95.9%; Pred. No. 1.1e-96;
 Matches 398; Conservative 0; Mismatches 12; Indels 5; Gaps 4;
 Qy 3 AACGTACAGACAGCTGCAAGTGGAGTTACGGATTGTAGAAAGCATCCTCATCTTG 62
 Db 292 AACGTACAGACAGCTGCAAGTGGAGTTACGGATTGTAGAAAGCATCCTCATCTTG 350
 Qy 63 TTGATATCTGGATAATGATCGAAAGCTTCGGAGACAATGGCTGGACCA 122
 Db 351 TTGATATCTGGATAATGATCGAAAGCTTCGGAGACAATGGCTGGACCA 410

RESULT 4
 BB642867
 LOCUS BB642867 RIKEN full-length enriched, adult retina Mus musculus cDNA
 DEFINITION clone A93104E03 5', mRNA sequence.
 ACCESSION BB642867
 VERSION 1 GI:16477625
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 676)
 AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanasaki,T., Hara,A.,
 Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,
 M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
 Okizaki,Y., Okido,T., Saito,R., Sakai,C., Sano,H., Sasakii,
 D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
 Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T.,
 Muramatsu,M. and Hayashizaki,Y.
 TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-reseqsc.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Carninci,P., Shibata,Y., Hayashizaki,Y., Sugahara,N., Sugahara,Y.,
 Konno,H., Fukunishi,Y., Muramatsu,M., and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
 Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,
 S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
 Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
 Y., and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo,S., Shinagawa,A., Saito,T., Kyosoya,H., Yananaka,I., Aizawa,
 K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
 Hayashizaki,Y.

BG700652	BG700652	791 bp	mRNA	linear	EST 07-MAY-2001	Db	573	AAAGCTATGTTAGCAACCATGTTGGTGGAAAATGGAGATATGGTTC	632
DEFINITION	602682269FL NIH_MGC_95	Homo sapiens	cdNA clone	IMAGE:4815064_5,		Qy	363	TOCCAGATGTCGATTCGAATGGCTTAATGATGTTNGAAAGCTTGACAGT	414
ACCESSION	BG700652								
VERSION	BG700652.1	GI:13970209				Db	633	TCCCCAGATGTCGATTCGAATGGCTTAATGATGTTAGCAAGTTGACAGT	684
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE	1 (bases 1 to 791)								
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/.							
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)								
JOURNAL	Unpublished (1999)								
COMMENT	Contact: Robert Strausberg, Ph.D.								
	Email: cgabs@mail.nih.gov								
	Tissue Procurement: Miklos Palkovits, M.D., Ph.D.								
	CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)								
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)								
	DNA Sequencing by: Incyte Genomics, Inc.								
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:								
	http://image.llnl.gov								
	Plate: LLM10711 row: 1 column: 17								
FEATURES	Location/Qualifiers								
source	1..791								
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	/db_xref="Taxon:9606"								
	/clones="IMAGE:4815064"								
	/clone.lib="NIH_MGC_95"								
	/tissue_type="hippocampus"								
	/lab_host="DH10B"								
	/note="Organ: brain; Vector: pBluescript KS+; Site_1: BamHI; Site_2: SalI-XbaI (gtcgag								
); Oligo-on primed using primer 5'-TTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation), library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."								
BASE COUNT	205 a 190 c 215 g 181 t								
ORIGIN									
	^ry Match	76.9%							
	^t Local Similarity	88.6%							
	^atches 365; Conservative 0; Mismatches 45; Indels 2; Gaps 2;								
Qy	3 AACGTACAGAACAGCTTGTGCAAGTTACCGATTGTCAGAAGCGATGCCAACCTTCATCTTG	62							
Db	275 AACCTTACAGAACAGCTGCAAAATA-CGAATTGTGCAAAAGATGCAACCTTCATCTTG	333							
Qy	63 TTGATATCGATATGATCGAAGTTTCGAGAAATGGCTTAACCGCTGGACCACA	122							
Db	334 TTGATATCGAACATGATGAACTCCGAGAACATGGCTTAATACACTGACCATA	393							
Qy	123 GCAAGGAGATCAGGGTGTGCCCTGGAGACCGTCATCTCGTCCATCTACATCAGTTG	182							
Db	394 CCACCGAGATCA-TGTGTGCCCTGGCTCGAAACTGTCATCCCTCCATCTACATCAGTTG	452							
Qy	183 AACAAAGCGCTTCTCTACTACCAAGATCAGGGTGGACGCCATAGTCCTACTC	242							
Db	453 AACAAAGCGCTTCTCTACTACCAAGATCAGGGTGGACGCCATAGTCCTACTC	512							
Qy	243 AATTCATGGTCGCGCTTACGAGTGGAGGGGAGGTGACCTGTTTCAGTT	302							
Db	513 AACCTTATGATGTCATGAGCTGGGGCGAGGCAAGTGGTATTTCACTT	572							
Qy	303 AAAGCTATGTTAGAACCATGTTGGTGGAAAAATGGTGGACAAATGGATACATTTC	362							
Db	406 AACTTTATGATTGCTGCATATGACAGTGGGGCAGGCAAGTGGTACGGTATTTCAGTT	465							

Qy	303	AAAGCTATGTTAGCAACCATTGTGGAAATTGAGATACTTC	362	Db	476	AACTAGGCCTTCATTCACTTGTGGACAAATTAGTGGGACAACTTC	535
Db	466	AAAGCTATGTTAGCAACCATTGTGGAAATTGAGATACTTC	525	Qy	243	AACTTCATGGTGGCGCTTACGGAGCTGGGGCGAGCTGGGACGGTTCAGTT	302
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Db	526	TCCCGATGTCAGATTCCAATGGCTTAATGATGTTGGAAATTGAGATACTTC	577	Qy	303	AAAGCTATGTTAGCAACCATTGTGGTGGAAAATGGGGACAAATTGAGATACTTC	362
RESULT 8				Db	596	AACTCTATTTAGAACCTATGTCAGCTGGGACAAATTGAGATACTTC	655
BO651659		BQ651659	932 bp	mRNA	EST	15-JUL-2002	QY_363 TCCCCAGATGTCAGATTCCAATGGCTTAATGATGTTGGGAAAGCTTGACCAAGT 414
LOCUS		AGENCOURT_8342332	NIH_MGC_100	Homo sapiens	cdNA clone IMAGE:6268278		Db_656 TCCCCAGATGTCAGATTCCAATGGCTTAATGATGTTGGGACAAATTGAGATACTTC
DEFINITION		5', mRNA sequence.					707
ORGANISM		human.					
SOURCE				RESULT 9			
ORGANISM		Homo sapiens		AL524324	367 bp	mRNA	EST 13-FEB-2001
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		LOCUS	AL524324	LTI_NFL003_NBC3	Homo sapiens cdNA clone CS0DC006YE12 5
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		DEFINITION	AL524324	prime mRNA sequence.	
AUTHORS		1 (bases 1 to 932)		ACCESSION	AL524324		
NIH_MGC		http://mgc.ncbi.nih.gov/		VERSION	AL524324.1	GI:127787817	
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)		KEYWORDS	EST		
JOURNAL		Unpublished (1999)		SOURCE	human.		
COMMENT		Contact: Robert Straussberg, Ph.D.		ORGANISM	Homo sapiens		
		Email: crapbs@email.nih.gov			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Tissue Procurement: CGAP (Stanford)			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
		cDNA Library Preparation: Rubin Laboratory		REFERENCE	1 (bases 1 to 967)		
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.		
		DNA Sequencing by: Agencourt Bioscience Corporation		TITLE	Full-length cDNA libraries and normalization		
		Clone distribution: MGC clone distribution information can be		JOURNAL	Unpublished (2001)		
		found through the I.M.A.G.E. Consortium/LLNL at:		COMMENT	Contact: Genoscope		
		http://image.llnl.gov			Genoscope - Centre National de Sequençage		
		Plate: LUCM2439 row: p column: 07			BP 191 91006 EVRY cedex - France		
		High quality sequence stop: 733.			Email: segre@genoscope.cns.fr , Web : www.genoscope.cns.fr		
FEATURES		Location/Qualifiers		FEATURES	Location/Qualifiers		
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		/clone lib="LTI_NFL003_NBC3"			/clone lib="LTI_NFL003_NBC3"		
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		/lab_host="DH10B" (phage-resistant)"			/tissue-type="neuroblastoma cells"		
		/note="Organ: liver. Vector: POFB7; Site1: XbaI; Site2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adapter: GGCACCAAG (6'). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP cDNA synthesis kit (Stratagene) and SuperScript II RT (Life Technologies). Note: this is a NIH_MGC Library."			/lab_host="DH10B"		
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ORIGIN		Query Match	76.9%		Score 318.4;	DB 9;	Length 967;
		Best Local Similarity	88.6%		Pred. No. 1.8e-87;		
		Matches	365;	Conservative	0; Mismatches 45;	Indels 45;	Gaps 2;
Qy	3	AACTAGACAGACAGCTGGAAATTGATCGAGATTACGGATTGTACAGAACCGATGCAACCTTCATCTTG	62	Query Match	76.9%	Score 318.4;	DB 9;
Db	298	AACTAGACAGACAGCTGGAAATTGATCGAGATTACGGATTGTACAGAACCGATGCAACCTTCATCTTG	356	Best Local Similarity	88.6%	Pred. No. 1.8e-87;	
Qy	63	TGTGATCTGGAAATTGATCGAGATTACGGATTGTACAGAACCGATGCAACCTTCATCTTG	122	Matches	365;	Conservative 0; Mismatches 45;	Indels 45;
Db	357	TGTGATCTGGAAATTGATCGAGATTACGGATTGTACAGAACCGATGCAACCTTCATCTTG	416	Qy	3 AACGTACAGAACAGCTGGAAATTGATCGAGATTACGGATTGTACAGAACCTTCATCTTG	62	
Qy	123	GCACGGAGATCAGGCCGTGTCAGCTGGCAACCGCTGATCGTCCATCTACTACAGTTG	182	Db	322 AACGTACAGAACAGCTGGAAATTGATCGAGATTACGGATTGTACAGAACCTTCATCTTG	380	
Db	417	CCACCGAGATCA-GTGTGTCGCCGCTCGAAGACTGTCACTCTCCATCTACTACAGTTG	475	Qy	63 TTGATATCTGGAAATTGATCGAGATTACGGATTGTACAGAACCTTCATCTTG	122	
Qy	183	AAACAGGCCATTCTACTACCAACGATCAGCTGGAGACTGTCATCGTCCATCTACTACAGTTG	242	Db	381 TTGATATCTGGAAATTGATCGAGATTACGGATTGTACAGAACCTTCATCTTG	440	
		BASE COUNT	229 a	250 c	256 g	227 t	5 others
ORIGIN		Query Match	76.9%		Score 318.4;	DB 9;	Length 967;
		Best Local Similarity	88.6%		Pred. No. 1.8e-87;		
		Matches	365;	Conservative	0; Mismatches 45;	Indels 45;	Gaps 2;
Qy	3	AACTAGACAGACAGCTGGAAATTGATCGAGATTACGGATTGTACAGAACCGATGCAACCTTCATCTTG	62	Query Match	76.9%	Score 318.4;	DB 9;
Db	298	AACTAGACAGACAGCTGGAAATTGATCGAGATTACGGATTGTACAGAACCGATGCAACCTTCATCTTG	356	Best Local Similarity	88.6%	Pred. No. 1.8e-87;	
Qy	63	TGTGATCTGGAAATTGATCGAGATTACGGATTGTACAGAACCGATGCAACCTTCATCTTG	122	Matches	365;	Conservative 0; Mismatches 45;	Indels 45;
Db	357	TGTGATCTGGAAATTGATCGAGATTACGGATTGTACAGAACCGATGCAACCTTCATCTTG	416	Qy	3 AACGTACAGAACAGCTGGAAATTGATCGAGATTACGGATTGTACAGAACCTTCATCTTG	62	
Qy	123	GCACGGAGATCAGGCCGTGTCAGCTGGCAACCGCTGATCGTCCATCTACTACAGTTG	182	Db	322 AACGTACAGAACAGCTGGAAATTGATCGAGATTACGGATTGTACAGAACCTTCATCTTG	380	
Db	417	CCACCGAGATCA-GTGTGTCGCCGCTCGAAGACTGTCACTCTCCATCTACTACAGTTG	475	Qy	63 TTGATATCTGGAAATTGATCGAGATTACGGATTGTACAGAACCTTCATCTTG	122	
Qy	183	AAACAGGCCATTCTACTACCAACGATCAGCTGGAGACTGTCATCGTCCATCTACTACAGTTG	242	Db	381 TTGATATCTGGAAATTGATCGAGATTACGGATTGTACAGAACCTTCATCTTG	440	
		BASE COUNT	229 a	250 c	256 g	227 t	5 others
ORIGIN		Query Match	76.9%		Score 318.4;	DB 9;	Length 967;
		Best Local Similarity	88.6%		Pred. No. 1.8e-87;		
		Matches	365;	Conservative	0; Mismatches 45;	Indels 45;	Gaps 2;
Qy	3	AACTAGACAGACAGCTGGAAATTGATCGAGATTACGGATTGTACAGAACCGATGCAACCTTCATCTTG	62	Query Match	76.9%	Score 318.4;	DB 9;
Db	298	AACTAGACAGACAGCTGGAAATTGATCGAGATTACGGATTGTACAGAACCGATGCAACCTTCATCTTG	356	Best Local Similarity	88.6%	Pred. No. 1.8e-87;	
Qy	63	TGTGATCTGGAAATTGATCGAGATTACGGATTGTACAGAACCGATGCAACCTTCATCTTG	122	Matches	365;	Conservative 0; Mismatches 45;	Indels 45;
Db	357	TGTGATCTGGAAATTGATCGAGATTACGGATTGTACAGAACCGATGCAACCTTCATCTTG	416	Qy	3 AACGTACAGAACAGCTGGAAATTGATCGAGATTACGGATTGTACAGAACCTTCATCTTG	62	
Qy	123	GCACGGAGATCAGGCCGTGTCAGCTGGCAACCGCTGATCGTCCATCTACTACAGTTG	182	Db	322 AACGTACAGAACAGCTGGAAATTGATCGAGATTACGGATTGTACAGAACCTTCATCTTG	380	
Db	417	CCACCGAGATCA-GTGTGTCGCCGCTCGAAGACTGTCACTCTCCATCTACTACAGTTG	475	Qy	63 TTGATATCTGGAAATTGATCGAGATTACGGATTGTACAGAACCTTCATCTTG	122	
Qy	183	AAACAGGCCATTCTACTACCAACGATCAGCTGGAGACTGTCATCGTCCATCTACTACAGTTG	242	Db	381 TTGATATCTGGAAATTGATCGAGATTACGGATTGTACAGAACCTTCATCTTG	440	

RESULT 15
 BG469017 830 bp mRNA linear EST 21-MAR-2001
 LOCUS 6021075/F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4644783 5', mRNA sequence.
 DEFINITION mRNA sequence.
 ACCESSION BG469017
 VERSION 1
 KEYWORDS EST
 SOURCE human
 ORGANISM Homo sapiens
 Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 830)
 REFERENCE NIH MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Straussberg, Ph.D.
 Email: csapbs@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrived by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://Image.llnl.gov
 Plate: LUCM1417 row: b column: 16
 High quality sequence stop: 646.
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 /note="Organ: Colon; Vector: P0R7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT Priming; Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG (G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"
 BASE COUNT
 ORIGIN
 Query Match 72.3% Score 299.4; DB 12; Length 830;
 1st Local Similarity 87.2%; Pred. No. 1..3e-81;
 patches 360; Conservative 0; Mismatches 50; Indels 3; Gaps 3;
 3;
 Qy 3 AACGTACAGAACAGCTTGGCAAGTTACGGATTTGACAGAACGGATGCAACCTTCATCTTG 62
 Db 265 AACTTAGAACAGCTGCAATTAA-CGATTTGACAAAGATGCAACCTTCATCTTG 323
 Qy 63 TTTGATATCTGGAAATATGATCGAACAGCTTCCGAGAACATGGCTTAACACGGGGACACA 122
 Db 324 TTTGATATCTGGAAATATGAGCCATTGAGCAGATGGCTTAACATGGACATA 383
 Qy 123 GCACGGGAGATCAGGGCTGAGACGGCTGAGACGGTCACTCTGTCATCTACTATCAGTTG 182
 Db 384 CCACCGAGATCA-GTGTGTCGCCCTCGAACATGTCATCCTCCATCTACTATCAGTTG 442
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 Db 443 ACAAAAGGGCTTCCTTCTACTACAGATCACGGCTGAGGGCAGCTGACGCTCCPACTC 502
 Qy 243 AATTTCATGGTGGCGCTTAACAGATCACGGCTGAGGGCAGCTGACGCTCCPACTC 302
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 Qy 303 AAAGCTATGTAGCAACCATGTTGGGAAATAATGCTGGACAATGAGATACTTTC 362